SEQUENCE LISTING

<110>	IMMUNE Carter Zhou,	, Pa	ul J	•	ON										
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Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala 85

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys 105 100

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn 120 115

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser 135

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala 155 150.

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn 170 165

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys 180 185

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr 200

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser 220 215 210

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Gly	Lys	Ser	Ala 340	Trp	Cys	Pro	Val	Glu 345	Ile	Ser	Lys	Thr	Val 350	Leu	Trp
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Ser	Ser	Pro 675	Glu	His	Leu	Gly	Leu 680	Glu	Pro	Gly	Glu	Lys 685	Val	Glu	Asp
Met	Pro 690	Lys	Pro	Pro	Leu	Pro 695	Gln	Glu	Gln	Ala	Thr 700	Asp	Pro	Leu	Val

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu 705 710 715 Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gln Thr 725 730 Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Gly Asp Arg Ser 740 Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly 755 760 765 Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly 780 770 775 Ile Ser Glu Lys Ser Lys Ser Ser Ser Phe His Pro Ala Pro Gly 785 790 795 800 Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser 805 810 Val Gly Pro Thr Tyr Met Arg Val Ser 820 <210> 3 <211> 327 <212> DNA <213> Artificial <220> <223> Light chain variable sequence <220> <221> CDS <222> (1)..(327) <400> 3 48 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly 96 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser 144 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 192 atc ttt ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55

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Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60	
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Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser 50 55 60

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Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu 70 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 90 Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys 100 <210> 13 <211> 327 <212> DNA <213> Artificial <220> <223> Light chain variable sequence <220> <221> CDS <222> (1)..(327) <400> 13 48 gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly 10 96 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser 144 tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu 192 atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 55 240 ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 70 288 cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 90 327 ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

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Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 50 55 60	192
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caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95	288
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Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly 15 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	-
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 Ala Thr Asn Tyr Ala Asp Ser Val Lys 60 Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	-

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Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                                                                       192
tca ggt att ggt act ggt gcc aca agc tat gca gac tcc gtg aag
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
                         55
                                                                       240
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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca
                                                                       288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc
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            100
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Val Ser Ser
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ggc cga tt Gly Arg Ph 65	c acc atc e Thr Ile	tcc aga Ser Arg 70	gac aat Asp Asn	Ala I	aag aac Lys Asn 75	tcc to Ser Lo	tg tat eu Tyr	ctt Leu 80	240
caa atg aa Gln Met As	c agc ctg n Ser Leu 85	aga gcc Arg Ala	gag gac Glu Asp	atg (Met 1 90	gct gtg Ala Val	tat to Tyr T	ac tgt yr Cys 95	gca Ala	288
aga ggg ag Arg Gly Ar	g tac tgg g Tyr Trp 100	tac aac Tyr Asn	aac tgg Asn Trp 105	Gly (cag gga Gln Gly	Thr L	tg gtc eu Val 10	acc Thr	336
gtc tcc tc Val Ser Se 11	r								345
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Ala Met Pl 39		. Arg Gln	Ala Pro	Gly	Lys Gly	Leu G 45	lu Trp	Val	
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Gly Arg Pl 65	e Thr Ile	e Ser Arg 70	Asp Ası	ı Ala	Lys Asn 75	Ser I	eu Tyr	Leu 80	
Gln Met A	sn Ser Let 85	ı Arg Ala	Glu Ası	90	Ala Val	Tyr 1	yr Cys 95	Ala	
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tec etg aga etc tec tgt gea gge tet gga ttc ace ttc agt aga aat
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta
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Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca
                                                                      288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
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                                                                      336
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc
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            100
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Val Ser Ser
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Ala	Met	Phe 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
Ser	Gly 50	Ile	Gly	Thr	Gly	Gly 55	Ala	Thr	Asn	Tyr	Ala 60	Asp	Ser	Val	Lys	
Gly 65	Arg	Phe	Thr	Ile	Ser 70	Arg	Asp	Asn	Ala	Lys 75	Asn	Ser	Leu	Туг	Leu 80	
Gln	Met	Asn	Ser	Leu 85	Arg	Ala	Glu	Asp	Met 90	Ala	Val	Tyr	Tyr	Cys 95	Ala	
Arg	Gly	Arg	Tyr 100	Tyr	Phe	Pro	Trp	Trp 105	Gly	Gln	Gly	Thr	Leu 110	Val	Thr	
Val	Ser	Ser 115														
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tco Ser	ctg Lev	g aga L Arg	cto Leu 20	tcc Ser	tgt Cys	gca Ala	ggc	tct Ser 25	gga Gly	tto Phe	aco Thr	tto Phe	agt Ser 30	aga Arg	aat Asn	96
gct Ala	ato Met	tto Phe 35	tgg Trp	gtt Val	. cgc . Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	a aaa y Lys	a ggt s Gly	cto Lev 45	g gag ı Glu	tgg Trp	g gta Val	144
tca Se:	ggt Gly	att / Ile	ggt Gly	act Thr	ggt Gly	ggt Gly 55	gco Ala	c aca	a aad Asi	c tat 1 Tyl	gca Ala	a gad a Asj	c tco p Sei	gtg Val	g aag L Lys	192
gg: Gl: 65	c cga y Arg	a tto g Phe	c acc	ato	tco Ser 70	aga Arg	gao Asi	c aat o Ası	gco n Ala	c aag a Lys 75	g aad s Asi	tce n Se:	c tto r Leo	g tat ı Tyi	ctt Leu 80	240

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Ala Met Phe T 35	Trp Val Arg	Gln Ala Pr 40	ro Gly Lys	Gly Leu Glu 45	Trp Val								
Ser Gly Ile G 50	Gly Thr Gly	Gly Ala Th	nr Asn Tyr	Ala Asp Ser 60	Val Lys								
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tcc ctg aga Ser Leu Arg	ctc tcc tgt Leu Ser Cys 20	gca ggc tct Ala Gly Ser 25	gga ttc acc Gly Phe Thr	ttc agt aga Phe Ser Arg 30	aat 96 Asn
gct atg ttc Ala Met Phe 35	tgg gtt cgc Trp Val Arg	cag gct cca Gln Ala Pro 40	gga aaa ggt Gly Lys Gly	ctg gag tgg Leu Glu Trp 45	gta 144 Val
tca ggt att Ser Gly Ile 50	ggt act ggt Gly Thr Gly	ggt gcc aca Gly Ala Thr 55	aac tat gca Asn Tyr Ala 60	gac tcc gtg Asp Ser Val	aag 192 Lys
ggc cga ttc Gly Arg Phe 65	acc atc tcc Thr Ile Ser 70	aga gac aat Arg Asp Asn	gcc aag aac Ala Lys Asn 75	tcc ttg tat Ser Leu Tyr	ctt 240 Leu 80
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aga ggg agg Arg Gly Arg	tac tgg tac Tyr Trp Tyr 100	ccg tgg tgg Pro Trp Trp	g ggc cag gga o Gly Gln Gly	acc ctg gtc Thr Leu Val 110	acc 336 Thr
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Ser Leu Arç	g Leu Ser Cy 20	s Ala Gly Se 25	r Gly Phe Thr	Phe Ser Arg	, Asn

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 90 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 Val Ser Ser 115 <210> 27 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) <400> 27 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly 10 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 144 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 288 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90

336 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 345 gtc tcc tca Val Ser Ser <210> 28 <211> 115 <212> PRT <213> Artificial <220> <223> Synthetic Construct <400> 28 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly 10 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 50 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 75 70 65 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 110 105 100 Val Ser Ser 115 <210> 29 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence

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gct Ala	atg Met	ttc Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144
tca Ser	ggt Gly 50	att Ile	ggt Gly	act Thr	ggt Gly	ggt Gly 55	gcc Ala	aca Thr	aac Asn	tat Tyr	gca Ala 60	gac Asp	tcc Ser	gtg Val	aag Lys	192
ggc Gly 65	cga Arg	ttc Phe	acc Thr	atc Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
caa Gln	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	atg Met 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga Arg	GJÀ âââ	agg Arg	tac Tyr 100	tgg Trp	ttc Phe	ccg Pro	tgg Trp	tgg Trp 105	ggc Gly	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	3,36
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Ala	Met	: Phe 35	Tr	Va]	Arg	g Glr	Ala 40	a Pro	Gl)	y Lys	: Gly	/ Let 45	ı Glu	ı Trg	Val	

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Ser	Leu	Arg	Leu 20	Ser	. Cys	Ala	Gly	Ser 25	Gly	Phe	Thr	· Phe	Ser 30	Arg	Asn	
Ala	Met	Phe	Trp	Val	. Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	45	ı Glu	Trp	Val	
Ser	Gly	Ile	Gly	Thr	Gly	Gly 55	Ala	Thi	Asr	∙ ТУх	Ala 60	a Asp	Ser	Val	Lys	

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 70 65 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 Val Ser Ser 115 <210> 35 <211> 345 <212> DNA Artificial <213> <220> <223> Heavy chain variable sequence <220> <221> CDS (1)..(345) <222> <400> 35 48 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly 10 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 25 20 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 tea ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 70 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336 Arg Gly Arg Tyr Trp Tyr Pro Trp Gly Gln Gly Thr Leu Val Thr 105 100 345 gtc tcc tca Val Ser Ser 115

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gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
tca ggt att ggt act ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	192
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	240
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95	288
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	336
gtc tcc tca Val Ser Ser 115	345
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Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn 20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 90 Arg Gly Arg Tyr Tyr Phe Pro Trp Gly Gln Gly Thr Leu Val Thr 105 100 Val Ser Ser 115 <210> 39 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly 10 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 240 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 75 288 caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100 345 gtc tcc tca Val Ser Ser 115 <210> 40

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Ala	atg Met	ttc Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144
tca Ser	ggt Gly 50	att Ile	ggt Gly	act Thr	ggt Gly	ggt Gly 55	gcc Ala	aca Thr	agc Ser	tat Tyr	gca Ala 60	gac Asp	tcc Ser	gtg Val	aag Lys	192
ggc Gly 65	cga Arg	ttc Phe	acc Thr	atc Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
caa Gln	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr,	tac Tyr	tgt Cys 95	gca Ala	288
aga Arg	GJÀ aaa	agg Arg	tac Tyr 100	tac Tyr	ttc Phe	ccg Pro	tgg Trp	tgg Trp 105	ggc Gly	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	336
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Ser	: Leu	Arg	Len	_												
			20	. Ser	· Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30	Arg	Asn	
Ala	a Met		20		•			25					30		Asn Val	
٠		: Ph∈ 35	20 Trp	Val	Arg	Gln	Ala 40	25 Pro	Gly	, Lys	Gly	Leu 45	30 Glu	Trp		
Sei	c Gly 50	Phe 35	20 Trp	Val	Arg	Gln Gly 55	Ala 40	25 Pro	Gly Ser	· Lys	Gly Ala 60	Leu 45 Asp	30 Glu Ser	Trp	Val	

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Val Ser Ser 115

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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn

20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt gcc aca agc tat gca gac tcc gtg aag

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys

50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

100 105 110

gtc tcc tca
Val Ser Ser
115

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gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tg Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu T 35 40 45	33 3	.44
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc g Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser V 50 55 60	-55	L92
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg t Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu T 65 70 75		240
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac t Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr C 85 90	.90 90	288
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg g Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu V 100 105 110	,	336
gtc tcc tca Val Ser Ser 115		345
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro 1 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser 20 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu 45 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser 60 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu	Arg Asn Trp Val Val Lys Tyr Leu 80	

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                                     10
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat
                                                                       96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
                                                                      144
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag
                                                                      192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
                         55
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
                                                                      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca
                                                                       288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc
                                                                       336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
                                 105
             100
                                                                       345
 gtc tcc tca
 Val Ser Ser
         115
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<400> 48

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr 100 105 110

Val Ser Ser 115

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<222> (1)..(345)

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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn

20
25
30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
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35 40 45

WO 2005/047331

Val Ser Ser

115

PCT/US2004/037242

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tcc c Ser L	tg a	Arg	ctc Leu 20	tcc Ser	tgt Cys	gca Ala	gcc Ala	tct Ser 25	gga Gly	ttc Phe	acc Thr	ttc Phe	agt Ser 30	aga Arg	aat Asn	96
gct a Ala M	íet	ttc Phe 35	tgg Trp	gtt Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	aaa Lys	ggt Gly	ctg Leu 45	gag Glu	tgg Trp	gta Val	144
tca g Ser G	ggt Gly	att Ile	ggt Gly	act Thr	ggt Gly	ggt Gly 55	gcc Ala	aca Thr	agc Ser	tat Tyr	gca Ala 60	gac Asp	tcc Ser	gtg Val	aag Lys	192
ggc o Gly 1 65	cga Arg	ttc Phe	acc Thr	atc Ile	tcc Ser 70	aga Arg	gac Asp	aat Asn	gcc Ala	aag Lys 75	aac Asn	tcc Ser	ttg Leu	tat Tyr	ctt Leu 80	240
caa a Gln I	atg Met	aac Asn	agc Ser	ctg Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga Arg	GJA aaa	agg Arg	tac Tyr 100	Trp	tac Tyr	ccg	tgg Trp	tgg Trp 105	, GT	caç Glr	g gga n Gly	acc Thr	cto Lev 110		acc Thr	336
gtc Val	tcc Ser	tca Ser 115	•											•		345
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95	
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	
Val Ser Ser 115	
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gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	240
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95	288
aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	336
gtc tcc tca Val Ser Ser 115	345
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95	
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	
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gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 50 55 60	192
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80	240
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95	288
aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 100 105 110	336
gtc tcc tca Val Ser Ser 115	345
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 20 25 . 30	

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caa atg Gln Met	aac ag Asn Se	c ctg r Leu 85	aga Arg	gcc Ala	gag Glu	gac Asp	acg Thr 90	gct Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys 95	gca Ala	288
aga ggg Arg Gly	agg ta Arg Ty 10	r Trp	ttc Phe	ccg Pro	tgg Trp	tgg Trp 105	ggc Gly	cag Gln	gga Gly	acc Thr	ctg Leu 110	gtc Val	acc Thr	336
gtc tcc Val Ser														345
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Ala Met	Phe Ti	mp Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
Ser Gly 50	Ile G	ly Thr	Gly	Gly 55	Ala	Thr	Asn	Tyr	Ala 60	Asp	Ser	Val	Lys	
Gly Arg 65	Phe T	ır Ile	Ser	Arg	Asp	Asn	Ala	Lys 75	Asn	Ser	Leu	Туr	Leu 80	
Gln Met	Asn S	er Leu 85	ı Arg	Ala	Glu	. Asp	Thr 90	Ala	. Val	Tyr	Tyr	Cys 95	Ala	
Arg Gly		yr Tr <u>r</u> 00) Phe	Pro	Trp	Trp 105		Gln	Gly	Thr	Leu 110	Val	Thr	
Val Ser	Ser 115													
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Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys 55 50 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 70 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr 105 100 Val Ser Ser 115 <210> 61 <211> 345 <212> DNA <213> Artificial <220> <223> Heavy chain variable sequence <220> <221> CDS <222> (1)..(345) <400> 61 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 10 96 tee etg aga etc tee tgt gea gee tet gga tte ace tte agt aga aat Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn 144 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys 240 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 288 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 90 85

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

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Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

PCT/US2004/037242 WO 2005/047331

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val 105 100 Thr Val Ser Ser 115 <210> 65 <211> 107 <212> PRT <213> Artificial <220> <223> 5A1 light chain variable region <400> 65 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 15 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr 25 20 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile 40 35 Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly 55 50 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro 80 75 70 65 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu 95 90 85 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys 105 100 !<210> 66 123 <211> <212> PRT <213> Artificial <220> <223> 5A1 heavy chain variable region <400> 66

10

15

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly

5

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe 20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val 35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95

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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 115 120

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<223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp 20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
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Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ser Ser Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys
85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser 115

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg 20 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 40 Tyr Ile Ala Ser Ile Led Gln Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro 75 70 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys 100 . 105 <210> 70 <211> 36 <212> DNA <213> Artificial <220> <223> Primers <220> <221> misc_featurė <222> (21)..(21) <223> N is A or G <220> <221> misc_feature <222> (24)..(24) <223> N is G or T <400> 70 36 gtcgacgccg ccaccatgga nttngggctg agctgg <210> 71 <211> 21 <212> DNA <213> Artificial <220> <223> Primers <400> 71 21 cttgaccagg cagcccaggg c

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205

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu

200

195

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser 290 295 300

i

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys 325